WHAT IS CLAIMED IS:

1. A method for screening nucleic acid binding elements (NABEs), said method comprising :

(a) contacting nucleic acid binding factors (NABFs) with NABEs under conditions to promote specific binding interactions therebetween;

(b) identifying complexes formed between said NABEs and said NABFs (NABE-NABF complexes);

(c) separating said NABF from said NABE-NABF complexes to obtain NABEs that bind to NABFs;

(d) marking said NABEs obtained in (c) (marked NABEs);

(e) contacting said marked NABEs with probes of known nucleic acid binding elements (NABE-ps) bound to a support under conditions to promote hybridization therebetween; and

(f) analyzing the hybridization in (e) in order to identify said marked NABEs.

2. A method according to claim 1, wherein said NABEs are extracted from a cell.

3. A method for screening nucleic acid binding elements (NABEs) that are differentially active in modified cells, said method comprising :

(a) contacting nucleic acid binding factors (NABFs) with NABEs derived from a modified cell under conditions to promote specific binding interactions therebetween;

(b) identifying complexes formed in (a) between said NABEs and said NABFs (NABE-NABF complexes);

(c) separating said NABFs from said NABE-NABF complex to obtain NABEs that bind to NABFs;

(d) marking said NABEs obtained in (c) (marked NABEs);

(e) contacting said marked NABEs with probes of known nucleic acid binding elements (NABE-ps) bound to a support under conditions to promote hybridization therebetween; and

(f) analyzing the hybridization in (e) in order to identify said marked NABEs that are differentially active in the modified cell.

4. A method according to claim 3, further comprising :

(g) contacting said NABFs with nucleic acid binding elements derived from a non-modified cell (non-modified cell NABEs) under conditions to promote specific binding interactions therebetween;

(h) identifying complexes formed in (i) between said non-modified cell NABEs and said NABFs (non-modified cell NABE-NABF complexes);

(i) separating said NABF from said non-modified cell NABE-NABF complex to obtain non-modified cell NABEs that bind with NABFs;

(j) marking said non-modified cell NABEs obtained in (i) with a marker that is different than the marker used to mark said modified cell NABEs (marked non-modified cell NABEs);

(k) contacting said marked non-modified cell NABEs with said NABE-ps bound to a support under conditions to promote hybridization; and

(l) comparing the amount of hybridization in (v) with the amount of hybridzation in (e) in order to identify the differentiated activity of said marked NABEs derived from the modified cell.

5. A method according to any one of claims 1-4, wherein said contacting in (a) includes incubating a pool of said NABEs with a pool of said NABFs in conditions conducive to the formation of said NABE-NABF complexes.

6. A method according to any one of claims 1-4, wherein said identification in (b) includes submitting said contacted NABFs and NABEs in (a) to an electrophoresis separation.

7. A method according to claim 6, wherein said electrophoresis separation is part of an electromobility shift assay (EMSA).

8. A method according to any one of claims 1-4, wherein said separation in (c) includes purification of said NABE-NABF complexes in order to eliminate the NABFs bound to said NABEs.

9. A method according to any one of claims 1-4, wherein said marking in (d) includes labelling said NABEs with a terminal primer marker.

10. A method according to claim 9, wherein said terminal primer marker is a fluorescent or radioactive label.

11. A method according to any one of claims 1-4, wherein said NABE-ps are bound to a microarray or microbeads.

12. A method according to any one of claims 1-4, wherein said NABEs contain binding sites for transcription factors.

13. A method as defined in claim 12, wherein said transcription factors include c-Rel, E2F-1, Egr-1, ER, NFκB p50, p53, Sp1 and YY1.